

Resource Summary Report

Generated by [Kravitz](#) on Sep 11, 2026

Genome Canada

RRID:SCR_000966

Type: Tool

Proper Citation

Genome Canada (RRID:SCR_000966)

Resource Information

URL: <http://www.genomecanada.ca/>

Proper Citation: Genome Canada (RRID:SCR_000966)

Description: Genome Canada is a non-profit organization that is funded by the Government of Canada. The organization funds large-scale science and technology to fuel innovation regarding genomics in multiple sectors such as health, agriculture and agri-food, forestry, fisheries and aquaculture, environment, energy and mining. They create partnerships at the program and research project levels.

Abbreviations: Genome Canada

Resource Type: nonprofit organization

Keywords: genome, genomics, funding, non profit, non-profit, innovation, health, agriculture, agri-food, agri food, forestry, fisheries, aquaculture, environment, energy, mining

Availability: Available to the research community

Resource Name: Genome Canada

Resource ID: SCR_000966

Alternate IDs: Crossref funder ID: 100008762, nlx_151964, Wikidata: Q3123000, ISNI: 0000 0001 0352 8618, grid.440163.4

Alternate URLs: <https://ror.org/029s29983>

Record Creation Time: 20220129T080204+0000

Record Last Update: 20260905T132427+0000

Ratings and Alerts

No rating or validation information has been found for Genome Canada.

No alerts have been found for Genome Canada.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

Listed below are recent publications. The full list is available at [Kravitz](#) .

VanInsberghe M, et al. (2018) Highly multiplexed single-cell quantitative PCR. PloS one, 13(1), e0191601.

Trost B, et al. (2016) Computational Analysis of the Predicted Evolutionary Conservation of Human Phosphorylation Sites. PloS one, 11(4), e0152809.

Chen YW, et al. (2016) A Systematic Review of Diagnostic Biomarkers of COPD Exacerbation. PloS one, 11(7), e0158843.

Chen CY, et al. (2016) YY1 binding association with sex-biased transcription revealed through X-linked transcript levels and allelic binding analyses. Scientific reports, 6, 37324.

Wang Y, et al. (2015) Whole genome SNP genotype piecemeal imputation. BMC bioinformatics, 16, 340.

Nambeesan SU, et al. (2015) Association mapping in sunflower (*Helianthus annuus* L.) reveals independent control of apical vs. basal branching. BMC plant biology, 15, 84.

Butterfield YS, et al. (2014) JAGuarR: junction alignments to genome for RNA-seq reads. PloS one, 9(7), e102398.

Pinzon-Latorre D, et al. (2014) Pectinmethylesterases (PME) and pectinmethylesterase inhibitors (PMEI) enriched during phloem fiber development in flax (*Linum usitatissimum*). PloS one, 9(8), e105386.

van Bakel H, et al. (2010) Most "dark matter" transcripts are associated with known genes. PLoS biology, 8(5), e1000371.

Wagner JR, et al. (2010) Computational analysis of whole-genome differential allelic expression data in human. PLoS computational biology, 6(7), e1000849.

Rellos P, et al. (2010) Structure of the CaMKII δ /calmodulin complex reveals the molecular mechanism of CaMKII kinase activation. PLoS biology, 8(7), e1000426.